

10/554561

2005 OCT 25 10:25:00

1 / 13

SEQUENCE LISTING

<110> YOUSUKE, EBINA
TOSHIYUKI, OBATA
MEDICAL AND BIOLOGICAL LABORATORIES CO., LTD.

<120> METHOD FOR DETERMINATION OF INSULIN RECEPTOR ALPHA SUBUNIT

<130> M3-A0301Y1P

<150> JP 2003-121955
<151> 2003-04-25

<150> JP 2003-433303
<151> 2003-12-26

<160> 2

<170> PatentIn version 3.1

<210> 1
<211> 2859
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> (1)..(81)
<223>

<220>
<221> CDS
<222> (1)..(2859)
<223>

<220>

<221> mat_peptide

<222> (82).. (926)

<223>

<400> 1

atg ggc acc ggg ggc cgg cgg ggg gcg gcg gcc gcg ccg ctg ctg gtg	48
Met Gly Thr Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val	
-25 -20 -15	
gcg gtg gcc gcg ctg cta ctg ggc gcc gcg ggc cac ctg tac ccc gga	96
Ala Val Ala Ala Leu Leu Leu Gly Ala Ala Gly His Leu Tyr Pro Gly	
-10 -5 -1 1 5	
gag gtg tgt ccc ggc atg gat atc cgg aac aac ctc act agg ttg cat	144
Glu Val Cys Pro Gly Met Asp Ile Arg Asn Asn Leu Thr Arg Leu His	
10 15 20	
gag ctg gag aat tgc tct gtc atc gaa gga cac ttg cag ata ctc ttg	192
Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His Leu Gln Ile Leu Leu	
25 30 35	
atg ttc aaa acg agg ccc gaa gat ttc cga gac ctc agt ttc ccc aaa	240
Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp Leu Ser Phe Pro Lys	
40 45 50	
ctc atc atg atc act gat tac ttg ctg ctc ttc cgg gtc tat ggg ctc	288
Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu	
55 60 65	
gag agc ctg aag gac ctg ttc ccc aac ctc acg gtc atc cgg gga tca	336
Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Ser	
70 75 80 85	
cga ctg ttc ttt aac tac gcg ctg gtc atc ttc gag atg gtt cac ctc	384
Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe Glu Met Val His Leu	
90 95 100	

aag gaa ctc ggc ctc tac aac ctg atg aac atc acc cgg ggt tct gtc	432
Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile Thr Arg Gly Ser Val	
105 110 115	
cgc atc gag aag aac aat gag ctc tgt tac ttg gcc act atc gac tgg	480
Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu Ala Thr Ile Asp Trp	
120 125 130	
tcc cgt atc ctg gat tcc gtg gag gat aat cac atc gtg ttg aac aaa	528
Ser Arg Ile Leu Asp Ser Val Glu Asp Asn His Ile Val Leu Asn Lys	
135 140 145	
gat gac aac gag gag tgt gga gac atc tgt ccg ggt acc gcg aag ggc	576
Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro Gly Thr Ala Lys Gly	
150 155 160 165	
aag acc aac tgc ccc gcc acc gtc atc aac ggg cag ttt gtc gaa cga	624
Lys Thr Asn Cys Pro Ala Thr Val Ile Asn Gly Gln Phe Val Glu Arg	
170 175 180	
tgt tgg act cat agt cac tgc cag aaa gtt tgc ccg acc atc tgt aag	672
Cys Trp Thr His Ser His Cys Gln Lys Val Cys Pro Thr Ile Cys Lys	
185 190 195	
tca cac ggc tgc acc gcc gaa ggc ctc tgt tgc cac agc gag tgc ctg	720
Ser His Gly Cys Thr Ala Glu Gly Leu Cys Cys His Ser Glu Cys Leu	
200 205 210	
ggc aac tgt tct cag ccc gac gac ccc acc aag tgc gtg gcc tgc cgc	768
Gly Asn Cys Ser Gln Pro Asp Asp Pro Thr Lys Cys Val Ala Cys Arg	
215 220 225	
aac ttc tac ctg gac ggc agg tgt gtg gag acc tgc ccg ccc ccg tac	816
Asn Phe Tyr Leu Asp Gly Arg Cys Val Glu Thr Cys Pro Pro Pro Tyr	
230 235 240 245	

tac cac ttc cag gac tgg cgc tgt gtg aac ttc agc ttc tgc cag gac	864
Tyr His Phe Gln Asp Trp Arg Cys Val Asn Phe Ser Phe Cys Gln Asp	
250 255 260	
ctg cac cac aaa tgc aag aac tcg cgg agg cag ggc tgc cac caa tac	912
Leu His His Lys Cys Lys Asn Ser Arg Arg Gln Gly Cys His Gln Tyr	
265 270 275	
gtc att cac aac aac aag tgc atc cct gag tgt ccc tcc ggg tac acg	960
Val Ile His Asn Asn Lys Cys Ile Pro Glu Cys Pro Ser Gly Tyr Thr	
280 285 290	
atg aat tcc agc aac ttg ctg tgc acc cca tgc ctg ggt ccc tgt ccc	1008
Met Asn Ser Ser Asn Leu Leu Cys Thr Pro Cys Leu Gly Pro Cys Pro	
295 300 305	
aag gtg tgc cac ctc cta gaa ggc gag aag acc atc gac tcg gtg acg	1056
Lys Val Cys His Leu Leu Glu Gly Glu Lys Thr Ile Asp Ser Val Thr	
310 315 320 325	
tct gcc cag gag ctc cga gga tgc acc gtc atc aac ggg agt ctg atc	1104
Ser Ala Gln Glu Leu Arg Gly Cys Thr Val Ile Asn Gly Ser Leu Ile	
330 335 340	
atc aac att cga gga ggc aac aat ctg gca gct gag cta gaa gcc aac	1152
Ile Asn Ile Arg Gly Gly Asn Asn Leu Ala Ala Glu Leu Glu Ala Asn	
345 350 355	
ctc ggc ctc att gaa gaa att tca ggg tat cta aaa atc cgc cga tcc	1200
Leu Gly Leu Ile Glu Glu Ile Ser Gly Tyr Leu Lys Ile Arg Arg Ser	
360 365 370	
tac gct ctg gtg tca ctt tcc ttc ttc cgg aag tta cgt ctg att cga	1248
Tyr Ala Leu Val Ser Leu Ser Phe Phe Arg Lys Leu Arg Leu Ile Arg	
375 380 385	

gga gag acc ttg gaa att ggg aac tac tcc ttc tat gcc ttg gac aac	1296
Gly Glu Thr Leu Glu Ile Gly Asn Tyr Ser Phe Tyr Ala Leu Asp Asn	
390 395 400 405	
cag aac cta agg cag ctc tgg gac tgg agc aaa cac aac ctc acc acc	1344
Gln Asn Leu Arg Gln Leu Trp Asp Trp Ser Lys His Asn Leu Thr Thr	
410 415 420	
act cag ggg aaa ctc ttc ttc cac tat aac ccc aaa ctc tgc ttg tca	1392
Thr Gln Gly Lys Leu Phe Phe His Tyr Asn Pro Lys Leu Cys Leu Ser	
425 430 435	
gaa atc cac aag atg gaa gaa gtt tca gga acc aag ggg cgc cag gag	1440
Glu Ile His Lys Met Glu Glu Val Ser Gly Thr Lys Gly Arg Gln Glu	
440 445 450	
aga aac gac att gcc ctg aag acc aat ggg gac aag gca tcc tgt gaa	1488
Arg Asn Asp Ile Ala Leu Lys Thr Asn Gly Asp Lys Ala Ser Cys Glu	
455 460 465	
aat gag tta ctt aaa ttt tct tac att cgg aca tct ttt gac aag atc	1536
Asn Glu Leu Leu Lys Phe Ser Tyr Ile Arg Thr Ser Phe Asp Lys Ile	
470 475 480 485	
ttg ctg aga tgg gag ccg tac tgg ccc ccc gac ttc cga gac ctc ttg	1584
Leu Leu Arg Trp Glu Pro Tyr Trp Pro Pro Asp Phe Arg Asp Leu Leu	
490 495 500	
ggg ttc atg ctg ttc tac aaa gag gcc cct tat cag aat gtg acg gag	1632
Gly Phe Met Leu Phe Tyr Lys Glu Ala Pro Tyr Gln Asn Val Thr Glu	
505 510 515	
ttc gat ggg cag gat gcg tgt ggt tcc aac agt tgg acg gtg gta gac	1680
Phe Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser Trp Thr Val Val Asp	
520 525 530	

att gac cca ccc ctg agg tcc aac gac ccc aaa tca cag aac cac cca	1728
Ile Asp Pro Pro Leu Arg Ser Asn Asp Pro Lys Ser Gln Asn His Pro	
535 540 545	
ggg tgg ctg atg cgg ggt ctc aag ccc tgg acc cag tat gcc atc ttt	1776
Gly Trp Leu Met Arg Gly Leu Lys Pro Trp Thr Gln Tyr Ala Ile Phe	
550 555 560 565	
gtg aag acc ctg gtc acc ttt tcg gat gaa cgc cgg acc tat ggg gcc	1824
Val Lys Thr Leu Val Thr Phe Ser Asp Glu Arg Arg Thr Tyr Gly Ala	
570 575 580	
aag agt gac atc att tat gtc cag aca gat gcc acc aac ccc tct gtg	1872
Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala Thr Asn Pro Ser Val	
585 590 595	
ccc ctg gat cca atc tca gtg tct aac tca tca tcc cag att att ctg	1920
Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser Ser Gln Ile Ile Leu	
600 605 610	
aag tgg aaa cca ccc tcc gac ccc aat ggc aac atc acc cac tac ctg	1968
Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn Ile Thr His Tyr Leu	
615 620 625	
gtt ttc tgg gag agg cag gcg gaa gac agt gag ctg ttc gag ctg gat	2016
Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu Leu Phe Glu Leu Asp	
630 635 640 645	
tat tgc ctc aaa ggg ctg aag ctg ccc tcg agg acc tgg tct cca cca	2064
Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg Thr Trp Ser Pro Pro	
650 655 660	
ttc gag tct gaa gat tct cag aag cac aac cag agt gag tat gag gat	2112
Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln Ser Glu Tyr Glu Asp	
665 670 675	

tcg gcc ggc gaa tgc tgc tcc tgt cca aag aca gac tct cag atc ctg	2160
Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr Asp Ser Gln Ile Leu	
680 685 690	
aag gag ctg gag gag tcc tcg ttt agg aag acg ttt gag gat tac ctg	2208
Lys Glu Leu Glu Glu Ser Ser Phe Arg Lys Thr Phe Glu Asp Tyr Leu	
695 700 705	
cac aac gtg gtt ttc gtc ccc aga aaa acc tct tca ggc act ggt gcc	2256
His Asn Val Val Phe Val Pro Arg Lys Thr Ser Ser Gly Thr Gly Ala	
710 715 720 725	
gag gac cct agg cca tct cgg aaa cgc agg tcc ctt ggc gat gtt ggg	2304
Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly	
730 735 740	
aat gtg acg gtg gcc gtg ccc acg gtg gca gct ttc ccc aac act tcc	2352
Asn Val Thr Val Ala Val Pro Thr Val Ala Ala Phe Pro Asn Thr Ser	
745 750 755	
tcg acc agc gtg ccc acg agt ccg gag gag cac agg cct ttt gag aag	2400
Ser Thr Ser Val Pro Thr Ser Pro Glu Glu His Arg Pro Phe Glu Lys	
760 765 770	
gtg gtg aac aag gag tcg ctg gtc atc tcc ggc ttg cga cac ttc acg	2448
Val Val Asn Lys Glu Ser Leu Val Ile Ser Gly Leu Arg His Phe Thr	
775 780 785	
ggc tat cgc atc gag ctg cag gct tgc aac cag gac acc cct gag gaa	2496
Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn Gln Asp Thr Pro Glu Glu	
790 795 800 805	
cgg tgc agt gtg gca gcc tac gtc agt gcg agg acc atg cct gaa gcc	2544
Arg Cys Ser Val Ala Ala Tyr Val Ser Ala Arg Thr Met Pro Glu Ala	
810 815 820	

aag gct gat gac att gtt ggc cct gtg acg cat gaa atc ttt gag aac	2592
Lys Ala Asp Asp Ile Val Gly Pro Val Thr His Glu Ile Phe Glu Asn	
825 830 835	
aac gtc gtc cac ttg atg tgg cag gag ccg aag gag ccc aat ggt ctg	2640
Asn Val Val His Leu Met Trp Gln Glu Pro Lys Glu Pro Asn Gly Leu	
840 845 850	
atc gtg ctg tat gaa gtg agt tat cgg cga tat ggt gat gag gag ctg	2688
Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg Tyr Gly Asp Glu Glu Leu	
855 860 865	
cat ctc tgc gtc tcc cgc aag cac ttc gct ctg gaa cgg ggc tgc agg	2736
His Leu Cys Val Ser Arg Lys His Phe Ala Leu Glu Arg Gly Cys Arg	
870 875 880 885	
ctg cgt ggg ctg tca ccg ggg aac tac agc gtg cga atc cgg gcc acc	2784
Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser Val Arg Ile Arg Ala Thr	
890 895 900	
tcc ctt gcg ggc aac ggc tct tgg acg gaa ccc acc tat ttc tac gtg	2832
Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu Pro Thr Tyr Phe Tyr Val	
905 910 915	
aca gac tat tta gac gtc ccg tca aat	2859
Thr Asp Tyr Leu Asp Val Pro Ser Asn	
920 925	

<210> 2

<211> 953

<212> PRT

<213> Homo sapiens

<400> 2

Met Gly Thr Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val
 -25 -20 -15

Ala Val Ala Ala Leu Leu Leu Gly Ala Ala Gly His Leu Tyr Pro Gly
 -10 -5 -1 1 5

Glu Val Cys Pro Gly Met Asp Ile Arg Asn Asn Leu Thr Arg Leu His
 10 15 20

Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His Leu Gln Ile Leu Leu
 25 30 35

Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp Leu Ser Phe Pro Lys
 40 45 50

Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu
 55 60 65

Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Ser
 70 75 80 85

Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe Glu Met Val His Leu
 90 95 100

Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile Thr Arg Gly Ser Val
 105 110 115

Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu Ala Thr Ile Asp Trp
 120 125 130

Ser Arg Ile Leu Asp Ser Val Glu Asp Asn His Ile Val Leu Asn Lys
 135 140 145

Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro Gly Thr Ala Lys Gly
 150 155 160 165

10 / 13

Lys Thr Asn Cys Pro Ala Thr Val Ile Asn Gly Gln Phe Val Glu Arg
170 175 180

Cys Trp Thr His Ser His Cys Gln Lys Val Cys Pro Thr Ile Cys Lys
185 190 195

Ser His Gly Cys Thr Ala Glu Gly Leu Cys Cys His Ser Glu Cys Leu
200 205 210

Gly Asn Cys Ser Gln Pro Asp Asp Pro Thr Lys Cys Val Ala Cys Arg
215 220 225

Asn Phe Tyr Leu Asp Gly Arg Cys Val Glu Thr Cys Pro Pro Pro Tyr
230 235 240 245

Tyr His Phe Gln Asp Trp Arg Cys Val Asn Phe Ser Phe Cys Gln Asp
250 255 260

Leu His His Lys Cys Lys Asn Ser Arg Arg Gln Gly Cys His Gln Tyr
265 270 275

Val Ile His Asn Asn Lys Cys Ile Pro Glu Cys Pro Ser Gly Tyr Thr
280 285 290

Met Asn Ser Ser Asn Leu Leu Cys Thr Pro Cys Leu Gly Pro Cys Pro
295 300 305

Lys Val Cys His Leu Leu Glu Gly Glu Lys Thr Ile Asp Ser Val Thr
310 315 320 325

Ser Ala Gln Glu Leu Arg Gly Cys Thr Val Ile Asn Gly Ser Leu Ile
330 335 340

Ile Asn Ile Arg Gly Gly Asn Asn Leu Ala Ala Glu Leu Glu Ala Asn
345 350 355

1 1 / 1 3

Leu Gly Leu Ile Glu Glu Ile Ser Gly Tyr Leu Lys Ile Arg Arg Ser
360 365 370

Tyr Ala Leu Val Ser Leu Ser Phe Phe Arg Lys Leu Arg Leu Ile Arg
375 380 385

Gly Glu Thr Leu Glu Ile Gly Asn Tyr Ser Phe Tyr Ala Leu Asp Asn
390 395 400 405

Gln Asn Leu Arg Gln Leu Trp Asp Trp Ser Lys His Asn Leu Thr Thr
410 415 420

Thr Gln Gly Lys Leu Phe Phe His Tyr Asn Pro Lys Leu Cys Leu Ser
425 430 435

Glu Ile His Lys Met Glu Glu Val Ser Gly Thr Lys Gly Arg Gln Glu
440 445 450

Arg Asn Asp Ile Ala Leu Lys Thr Asn Gly Asp Lys Ala Ser Cys Glu
455 460 465

Asn Glu Leu Leu Lys Phe Ser Tyr Ile Arg Thr Ser Phe Asp Lys Ile
470 475 480 485

Leu Leu Arg Trp Glu Pro Tyr Trp Pro Pro Asp Phe Arg Asp Leu Leu
490 495 500

Gly Phe Met Leu Phe Tyr Lys Glu Ala Pro Tyr Gln Asn Val Thr Glu
505 510 515

Phe Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser Trp Thr Val Val Asp
520 525 530

Ile Asp Pro Pro Leu Arg Ser Asn Asp Pro Lys Ser Gln Asn His Pro
535 540 545

1 2 / 1 3

Gly Trp Leu Met Arg Gly Leu Lys Pro Trp Thr Gln Tyr Ala Ile Phe
550 555 560 565

Val Lys Thr Leu Val Thr Phe Ser Asp Glu Arg Arg Thr Tyr Gly Ala
570 575 580

Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala Thr Asn Pro Ser Val
585 590 595

Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser Ser Gln Ile Ile Leu
600 605 610

Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn Ile Thr His Tyr Leu
615 620 625

Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu Leu Phe Glu Leu Asp
630 635 640 645

Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg Thr Trp Ser Pro Pro
650 655 660

Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln Ser Glu Tyr Glu Asp
665 670 675

Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr Asp Ser Gln Ile Leu
680 685 690

Lys Glu Leu Glu Glu Ser Ser Phe Arg Lys Thr Phe Glu Asp Tyr Leu
695 700 705

His Asn Val Val Phe Val Pro Arg Lys Thr Ser Ser Gly Thr Gly Ala
710 715 720 725

Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly
730 735 740

1 3 / 1 3

Asn Val Thr Val Ala Val Pro Thr Val Ala Ala Phe Pro Asn Thr Ser
745 750 755

Ser Thr Ser Val Pro Thr Ser Pro Glu Glu His Arg Pro Phe Glu Lys
760 765 770

Val Val Asn Lys Glu Ser Leu Val Ile Ser Gly Leu Arg His Phe Thr
775 780 785

Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn Gln Asp Thr Pro Glu Glu
790 795 800 805

Arg Cys Ser Val Ala Ala Tyr Val Ser Ala Arg Thr Met Pro Glu Ala
810 815 820

Lys Ala Asp Asp Ile Val Gly Pro Val Thr His Glu Ile Phe Glu Asn
825 830 835

Asn Val Val His Leu Met Trp Gln Glu Pro Lys Glu Pro Asn Gly Leu
840 845 850

Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg Tyr Gly Asp Glu Glu Leu
855 860 865

His Leu Cys Val Ser Arg Lys His Phe Ala Leu Glu Arg Gly Cys Arg
870 875 880 885

Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser Val Arg Ile Arg Ala Thr
890 895 900

Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu Pro Thr Tyr Phe Tyr Val
905 910 915

Thr Asp Tyr Leu Asp Val Pro Ser Asn
920 925

10/554561

SEQUENCE LISTING

<110> Ebina, Yousuke
Obata, Toshiyuki
Okamoto, Eiji

JC20 Rec'd PCT/PTO 25 OCT 2005

<120> METHODS FOR MEASURING THE INSULIN
RECEPTOR ALPHA SUBUNIT

<130> 082368-006600US

<150> PCT/JP2004/005412
<151> 2004-04-15

<150> JP 2003-121955
<151> 2003-04-25

<150> JP 2003-433303
<151> 2003-12-26

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2859
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> (1)...(81)

<221> CDS
<222> (1)...(2859)

<221> mat_peptide
<222> (82)...(926)

<400> 1
atg ggc acc ggg ggc cgg cgg ggg gcg gcg gcc gcg ccg ctg ctg gtg 48
Met Gly Thr Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val
-25 -20 -15

gcg gtg gcc gcg ctg cta ctg ggc gcc gcg ggc cac ctg tac ccc gga 96
Ala Val Ala Ala Leu Leu Gly Ala Ala Gly His Leu Tyr Pro Gly
-10 -5 1 5

gag gtg tgt ccc ggc atg gat atc cgg aac aac ctc act agg ttg cat 144
Glu Val Cys Pro Gly Met Asp Ile Arg Asn Asn Leu Thr Arg Leu His
10 15 20

gag ctg gag aat tgc tct gtc atc gaa gga cac ttg cag ata ctc ttg 192
Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His Leu Gln Ile Leu Leu
25 30 35

atg ttc aaa acg agg ccc gaa gat ttc cga gac ctc agt ttc ccc aaa 240
Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp Leu Ser Phe Pro Lys
40 45 50

ctc atc atg atc act gat tac ttg ctg ctc ttc cgg gtc tat ggg ctc	288
Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu	
55 60 65	
gag agc ctg aag gac ctg ttc ccc aac ctc acg gtc atc cgg gga tca	336
Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Ser	
70 75 80 85	
cga ctg ttc ttt aac tac gcg ctg gtc atc ttc gag atg gtt cac ctc	384
Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe Glu Met Val His Leu	
90 95 100	
aag gaa ctc ggc ctc tac aac ctg atg aac atc acc cgg ggt tct gtc	432
Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile Thr Arg Gly Ser Val	
105 110 115	
cgc atc gag aag aac aat gag ctc tgt tac ttg gcc act atc gac tgg	480
Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu Ala Thr Ile Asp Trp	
120 125 130	
tcc cgt atc ctg gat tcc gtg gag gat aat cac atc gtg ttg aac aaa	528
Ser Arg Ile Leu Asp Ser Val Glu Asp Asn His Ile Val Leu Asn Lys	
135 140 145	
gat gac aac gag gag tgt gga gac atc tgt ccg ggt acc gcg aag ggc	576
Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro Gly Thr Ala Lys Gly	
150 155 160 165	
aag acc aac tgc ccc gcc acc gtc atc aac ggg cag ttt gtc gaa cga	624
Lys Thr Asn Cys Pro Ala Thr Val Ile Asn Gly Gln Phe Val Glu Arg	
170 175 180	
tgt tgg act cat agt cac tgc cag aaa gtt tgc ccg acc atc tgt aag	672
Cys Trp Thr His Ser His Cys Gln Lys Val Cys Pro Thr Ile Cys Lys	
185 190 195	
tca cac ggc tgc acc gcc gaa ggc ctc tgt tgc cac agc gag tgc ctg	720
Ser His Gly Cys Thr Ala Glu Gly Leu Cys Cys His Ser Glu Cys Leu	
200 205 210	
ggc aac tgt tct cag ccc gac gac ccc acc aag tgc gtg gcc tgc cgc	768
Gly Asn Cys Ser Gln Pro Asp Asp Pro Thr Lys Cys Val Ala Cys Arg	
215 220 225	
aac ttc tac ctg gac ggc agg tgt gtg gag acc tgc ccg ccc ccg tac	816
Asn Phe Tyr Leu Asp Gly Arg Cys Val Glu Thr Cys Pro Pro Pro Tyr	
230 235 240 245	
tac cac ttc cag gac tgg cgc tgt gtg aac ttc agc ttc tgc cag gac	864
Tyr His Phe Gln Asp Trp Arg Cys Val Asn Phe Ser Phe Cys Gln Asp	
250 255 260	
ctg cac cac aaa tgc aag aac tcg cgg agg cag ggc tgc cac caa tac	912
Leu His His Lys Cys Lys Asn Ser Arg Arg Gln Gly Cys His Gln Tyr	
265 270 275	
gtc att cac aac aac aag tgc atc cct gag tgt ccc tcc ggg tac acg	960
Val Ile His Asn Asn Lys Cys Ile Pro Glu Cys Pro Ser Gly Tyr Thr	
280 285 290	
atg aat tcc agc aac ttg ctg tgc acc cca tgc ctg ggt ccc tgt ccc	1008

Met	Asn	Ser	Ser	Asn	Leu	Leu	Cys	Thr	Pro	Cys	Leu	Gly	Pro	Cys	Pro	
295						300					305					
aag	gtg	tgc	cac	ctc	cta	gaa	ggc	gag	aag	acc	atc	gac	tcg	gtg	acg	1056
Lys	Val	Cys	His	Leu	Leu	Glu	Gly	Glu	Lys	Thr	Ile	Asp	Ser	Val	Thr	
310					315					320					325	
tct	gcc	cag	gag	ctc	cga	gga	tgc	acc	gtc	atc	aac	ggg	agt	ctg	atc	1104
Ser	Ala	Gln	Glu	Leu	Arg	Gly	Cys	Thr	Val	Ile	Asn	Gly	Ser	Leu	Ile	
				330					335					340		
atc	aac	att	cga	gga	ggc	aac	aat	ctg	gca	gct	gag	cta	gaa	gcc	aac	1152
Ile	Asn	Ile	Arg	Gly	Gly	Asn	Asn	Leu	Ala	Ala	Glu	Leu	Glu	Ala	Asn	
			345					350					355			
ctc	ggc	ctc	att	gaa	gaa	att	tca	ggg	tat	cta	aaa	atc	cgc	cga	tcc	1200
Leu	Gly	Leu	Ile	Glu	Glu	Ile	Ser	Gly	Tyr	Leu	Lys	Ile	Arg	Arg	Ser	
		360					365					370				
tac	gct	ctg	gtg	tca	ctt	tcc	ttc	ttc	cgg	aag	tta	cgt	ctg	att	cga	1248
Tyr	Ala	Leu	Val	Ser	Leu	Ser	Phe	Phe	Arg	Lys	Leu	Arg	Leu	Ile	Arg	
	375					380					385					
gga	gag	acc	ttg	gaa	att	ggg	aac	tac	tcc	ttc	tat	gcc	ttg	gac	aac	1296
Gly	Glu	Thr	Leu	Glu	Ile	Gly	Asn	Tyr	Ser	Phe	Tyr	Ala	Leu	Asp	Asn	
390					395					400					405	
cag	aac	cta	agg	cag	ctc	tgg	gac	tgg	agc	aaa	cac	aac	ctc	acc	acc	1344
Gln	Asn	Leu	Arg	Gln	Leu	Trp	Asp	Trp	Ser	Lys	His	Asn	Leu	Thr	Thr	
				410					415					420		
act	cag	ggg	aaa	ctc	ttc	ttc	cac	tat	aac	ccc	aaa	ctc	tgc	ttg	tca	1392
Thr	Gln	Gly	Lys	Leu	Phe	Phe	His	Tyr	Asn	Pro	Lys	Leu	Cys	Leu	Ser	
			425					430					435			
gaa	atc	cac	aag	atg	gaa	gaa	gtt	tca	gga	acc	aag	ggg	cgc	cag	gag	1440
Glu	Ile	His	Lys	Met	Glu	Glu	Val	Ser	Gly	Thr	Lys	Gly	Arg	Gln	Glu	
		440					445					450				
aga	aac	gac	att	gcc	ctg	aag	acc	aat	ggg	gac	aag	gca	tcc	tgt	gaa	1488
Arg	Asn	Asp	Ile	Ala	Leu	Lys	Thr	Asn	Gly	Asp	Lys	Ala	Ser	Cys	Glu	
	455					460					465					
aat	gag	tta	ctt	aaa	ttt	tct	tac	att	cgg	aca	tct	ttt	gac	aag	atc	1536
Asn	Glu	Leu	Leu	Lys	Phe	Ser	Tyr	Ile	Arg	Thr	Ser	Phe	Asp	Lys	Ile	
470					475					480					485	
ttg	ctg	aga	tgg	gag	ccg	tac	tgg	ccc	ccc	gac	ttc	cga	gac	ctc	ttg	1584
Leu	Leu	Arg	Trp	Glu	Pro	Tyr	Trp	Pro	Pro	Asp	Phe	Arg	Asp	Leu	Leu	
				490					495					500		
ggg	ttc	atg	ctg	ttc	tac	aaa	gag	gcc	cct	tat	cag	aat	gtg	acg	gag	1632
Gly	Phe	Met	Leu	Phe	Tyr	Lys	Glu	Ala	Pro	Tyr	Gln	Asn	Val	Thr	Glu	
			505					510					515			
ttc	gat	ggg	cag	gat	gcg	tgt	ggt	tcc	aac	agt	tgg	acg	gtg	gta	gac	1680
Phe	Asp	Gly	Gln	Asp	Ala	Cys	Gly	Ser	Asn	Ser	Trp	Thr	Val	Val	Asp	
		520					525					530				
att	gac	cca	ccc	ctg	agg	tcc	aac	gac	ccc	aaa	tca	cag	aac	cac	cca	1728
Ile	Asp	Pro	Pro	Leu	Arg	Ser	Asn	Asp	Pro	Lys	Ser	Gln	Asn	His	Pro	

535	540	545	
ggg tgg ctg atg cgg ggt ctc aag ccc tgg acc cag tat gcc atc ttt Gly Trp Leu Met Arg Gly Leu Lys Pro Trp Thr Gln Tyr Ala Ile Phe 550 555 560 565			1776
gtg aag acc ctg gtc acc ttt tcg gat gaa cgc cgg acc tat ggg gcc Val Lys Thr Leu Val Thr Phe Ser Asp Glu Arg Arg Thr Tyr Gly Ala 570 575 580			1824
aag agt gac atc att tat gtc cag aca gat gcc acc aac ccc tct gtg Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala Thr Asn Pro Ser Val 585 590 595			1872
ccc ctg gat cca atc tca gtg tct aac tca tca tcc cag att att ctg Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser Ser Gln Ile Ile Leu 600 605 610			1920
aag tgg aaa cca ccc tcc gac ccc aat ggc aac atc acc cac tac ctg Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn Ile Thr His Tyr Leu 615 620 625			1968
gtt ttc tgg gag agg cag gcg gaa gac agt gag ctg ttc gag ctg gat Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu Leu Phe Glu Leu Asp 630 635 640 645			2016
tat tgc ctc aaa ggg ctg aag ctg ccc tcg agg acc tgg tct cca cca Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg Thr Trp Ser Pro Pro 650 655 660			2064
ttc gag tct gaa gat tct cag aag cac aac cag agt gag tat gag gat Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln Ser Glu Tyr Glu Asp 665 670 675			2112
tcg gcc ggc gaa tgc tgc tcc tgt cca aag aca gac tct cag atc ctg Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr Asp Ser Gln Ile Leu 680 685 690			2160
aag gag ctg gag gag tcc tcg ttt agg aag acg ttt gag gat tac ctg Lys Glu Leu Glu Glu Ser Ser Phe Arg Lys Thr Phe Glu Asp Tyr Leu 695 700 705			2208
cac aac gtg gtt ttc gtc ccc aga aaa acc tct tca ggc act ggt gcc His Asn Val Val Phe Val Pro Arg Lys Thr Ser Ser Gly Thr Gly Ala 710 715 720 725			2256
gag gac cct agg cca tct cgg aaa cgc agg tcc ctt ggc gat gtt ggg Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly 730 735 740			2304
aat gtg acg gtg gcc gtg ccc acg gtg gca gct ttc ccc aac act tcc Asn Val Thr Val Ala Val Pro Thr Val Ala Ala Phe Pro Asn Thr Ser 745 750 755			2352
tcg acc agc gtg ccc acg agt ccg gag gag cac agg cct ttt gag aag Ser Thr Ser Val Pro Thr Ser Pro Glu Glu His Arg Pro Phe Glu Lys 760 765 770			2400
gtg gtg aac aag gag tcg ctg gtc atc tcc ggc ttg cga cac ttc acg Val Val Asn Lys Glu Ser Leu Val Ile Ser Gly Leu Arg His Phe Thr			2448

775	780	785	
ggc tat cgc atc gag ctg cag gct tgc aac cag gac acc cct gag gaa			2496
Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn Gln Asp Thr Pro Glu Glu			
790	795	800	805
cgg tgc agt gtg gca gcc tac gtc agt gcg agg acc atg cct gaa gcc			2544
Arg Cys Ser Val Ala Ala Tyr Val Ser Ala Arg Thr Met Pro Glu Ala			
	810	815	820
aag gct gat gac att gtt ggc cct gtg acg cat gaa atc ttt gag aac			2592
Lys Ala Asp Asp Ile Val Gly Pro Val Thr His Glu Ile Phe Glu Asn			
	825	830	835
aac gtc gtc cac ttg atg tgg cag gag ccg aag gag ccc aat ggt ctg			2640
Asn Val Val His Leu Met Trp Gln Glu Pro Lys Glu Pro Asn Gly Leu			
	840	845	850
atc gtg ctg tat gaa gtg agt tat cgg cga tat ggt gat gag gag ctg			2688
Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg Tyr Gly Asp Glu Glu Leu			
	855	860	865
cat ctc tgc gtc tcc cgc aag cac ttc gct ctg gaa cgg ggc tgc agg			2736
His Leu Cys Val Ser Arg Lys His Phe Ala Leu Glu Arg Gly Cys Arg			
	870	875	880
ctg cgt ggg ctg tca ccg ggg aac tac agc gtg cga atc cgg gcc acc			2784
Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser Val Arg Ile Arg Ala Thr			
	890	895	900
tcc ctt gcg ggc aac ggc tct tgg acg gaa ccc acc tat ttc tac gtg			2832
Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu Pro Thr Tyr Phe Tyr Val			
	905	910	915
aca gac tat tta gac gtc ccg tca aat			2859
Thr Asp Tyr Leu Asp Val Pro Ser Asn			
	920	925	
<210> 2			
<211> 953			
<212> PRT			
<213> Homo sapiens			
<220>			
<221> SIGNAL			
<222> (1)...(27)			
<400> 2			
Met Gly Thr Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val			
	-25	-20	-15
Ala Val Ala Ala Leu Leu Leu Gly Ala Ala Gly His Leu Tyr Pro Gly			
	-10	-5	1
Glu Val Cys Pro Gly Met Asp Ile Arg Asn Asn Leu Thr Arg Leu His			
	10	15	20
Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His Leu Gln Ile Leu Leu			
	25	30	35
Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp Leu Ser Phe Pro Lys			
	40	45	50
Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu			

55	60	65
Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Ser		
70	75	80
Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe Glu Met Val His Leu		
	90	95
Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile Thr Arg Gly Ser Val		
	105	110
Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu Ala Thr Ile Asp Trp		
	120	125
Ser Arg Ile Leu Asp Ser Val Glu Asp Asn His Ile Val Leu Asn Lys		
	135	140
Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro Gly Thr Ala Lys Gly		
150	155	160
Lys Thr Asn Cys Pro Ala Thr Val Ile Asn Gly Gln Phe Val Glu Arg		
	170	175
Cys Trp Thr His Ser His Cys Gln Lys Val Cys Pro Thr Ile Cys Lys		
	185	190
Ser His Gly Cys Thr Ala Glu Gly Leu Cys Cys His Ser Glu Cys Leu		
	200	205
Gly Asn Cys Ser Gln Pro Asp Asp Pro Thr Lys Cys Val Ala Cys Arg		
	215	220
Asn Phe Tyr Leu Asp Gly Arg Cys Val Glu Thr Cys Pro Pro Pro Tyr		
230	235	240
Tyr His Phe Gln Asp Trp Arg Cys Val Asn Phe Ser Phe Cys Gln Asp		
	250	255
Leu His His Lys Cys Lys Asn Ser Arg Arg Gln Gly Cys His Gln Tyr		
	265	270
Val Ile His Asn Asn Lys Cys Ile Pro Glu Cys Pro Ser Gly Tyr Thr		
	280	285
Met Asn Ser Ser Asn Leu Leu Cys Thr Pro Cys Leu Gly Pro Cys Pro		
	295	300
Lys Val Cys His Leu Leu Glu Gly Glu Lys Thr Ile Asp Ser Val Thr		
310	315	320
Ser Ala Gln Glu Leu Arg Gly Cys Thr Val Ile Asn Gly Ser Leu Ile		
	330	335
Ile Asn Ile Arg Gly Gly Asn Asn Leu Ala Ala Glu Leu Glu Ala Asn		
	345	350
Leu Gly Leu Ile Glu Glu Ile Ser Gly Tyr Leu Lys Ile Arg Arg Ser		
	360	365
Tyr Ala Leu Val Ser Leu Ser Phe Phe Arg Lys Leu Arg Leu Ile Arg		
	375	380
Gly Glu Thr Leu Glu Ile Gly Asn Tyr Ser Phe Tyr Ala Leu Asp Asn		
390	395	400
Gln Asn Leu Arg Gln Leu Trp Asp Trp Ser Lys His Asn Leu Thr Thr		
	410	415
Thr Gln Gly Lys Leu Phe Phe His Tyr Asn Pro Lys Leu Cys Leu Ser		
	425	430
Glu Ile His Lys Met Glu Glu Val Ser Gly Thr Lys Gly Arg Gln Glu		
	440	445
Arg Asn Asp Ile Ala Leu Lys Thr Asn Gly Asp Lys Ala Ser Cys Glu		
	455	460
Asn Glu Leu Leu Lys Phe Ser Tyr Ile Arg Thr Ser Phe Asp Lys Ile		
470	475	480
Leu Leu Arg Trp Glu Pro Tyr Trp Pro Pro Asp Phe Arg Asp Leu Leu		
	490	495
Gly Phe Met Leu Phe Tyr Lys Glu Ala Pro Tyr Gln Asn Val Thr Glu		
	505	510
Phe Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser Trp Thr Val Val Asp		
	520	525
Ile Asp Pro Pro Leu Arg Ser Asn Asp Pro Lys Ser Gln Asn His Pro		
535	540	545

Gly	Trp	Leu	Met	Arg	Gly	Leu	Lys	Pro	Trp	Thr	Gln	Tyr	Ala	Ile	Phe
550					555					560					565
Val	Lys	Thr	Leu	Val	Thr	Phe	Ser	Asp	Glu	Arg	Arg	Thr	Tyr	Gly	Ala
				570					575						580
Lys	Ser	Asp	Ile	Ile	Tyr	Val	Gln	Thr	Asp	Ala	Thr	Asn	Pro	Ser	Val
			585					590					595		
Pro	Leu	Asp	Pro	Ile	Ser	Val	Ser	Asn	Ser	Ser	Ser	Gln	Ile	Ile	Leu
		600					605					610			
Lys	Trp	Lys	Pro	Pro	Ser	Asp	Pro	Asn	Gly	Asn	Ile	Thr	His	Tyr	Leu
	615					620					625				
Val	Phe	Trp	Glu	Arg	Gln	Ala	Glu	Asp	Ser	Glu	Leu	Phe	Glu	Leu	Asp
630					635					640					645
Tyr	Cys	Leu	Lys	Gly	Leu	Lys	Leu	Pro	Ser	Arg	Thr	Trp	Ser	Pro	Pro
				650					655					660	
Phe	Glu	Ser	Glu	Asp	Ser	Gln	Lys	His	Asn	Gln	Ser	Glu	Tyr	Glu	Asp
			665					670					675		
Ser	Ala	Gly	Glu	Cys	Cys	Ser	Cys	Pro	Lys	Thr	Asp	Ser	Gln	Ile	Leu
		680					685					690			
Lys	Glu	Leu	Glu	Glu	Ser	Ser	Phe	Arg	Lys	Thr	Phe	Glu	Asp	Tyr	Leu
	695					700					705				
His	Asn	Val	Val	Phe	Val	Pro	Arg	Lys	Thr	Ser	Ser	Gly	Thr	Gly	Ala
710					715					720					725
Glu	Asp	Pro	Arg	Pro	Ser	Arg	Lys	Arg	Arg	Ser	Leu	Gly	Asp	Val	Gly
				730					735					740	
Asn	Val	Thr	Val	Ala	Val	Pro	Thr	Val	Ala	Ala	Phe	Pro	Asn	Thr	Ser
			745					750					755		
Ser	Thr	Ser	Val	Pro	Thr	Ser	Pro	Glu	Glu	His	Arg	Pro	Phe	Glu	Lys
		760				765						770			
Val	Val	Asn	Lys	Glu	Ser	Leu	Val	Ile	Ser	Gly	Leu	Arg	His	Phe	Thr
	775					780					785				
Gly	Tyr	Arg	Ile	Glu	Leu	Gln	Ala	Cys	Asn	Gln	Asp	Thr	Pro	Glu	Glu
790					795					800					805
Arg	Cys	Ser	Val	Ala	Ala	Tyr	Val	Ser	Ala	Arg	Thr	Met	Pro	Glu	Ala
				810					815					820	
Lys	Ala	Asp	Asp	Ile	Val	Gly	Pro	Val	Thr	His	Glu	Ile	Phe	Glu	Asn
			825					830					835		
Asn	Val	Val	His	Leu	Met	Trp	Gln	Glu	Pro	Lys	Glu	Pro	Asn	Gly	Leu
		840				845						850			
Ile	Val	Leu	Tyr	Glu	Val	Ser	Tyr	Arg	Arg	Tyr	Gly	Asp	Glu	Glu	Leu
	855					860					865				
His	Leu	Cys	Val	Ser	Arg	Lys	His	Phe	Ala	Leu	Glu	Arg	Gly	Cys	Arg
870					875					880					885
Leu	Arg	Gly	Leu	Ser	Pro	Gly	Asn	Tyr	Ser	Val	Arg	Ile	Arg	Ala	Thr
				890					895					900	
Ser	Leu	Ala	Gly	Asn	Gly	Ser	Trp	Thr	Glu	Pro	Thr	Tyr	Phe	Tyr	Val
			905					910					915		
Thr	Asp	Tyr	Leu	Asp	Val	Pro	Ser	Asn							
		920					925								